R/qtl2

rewrite of a very old R package

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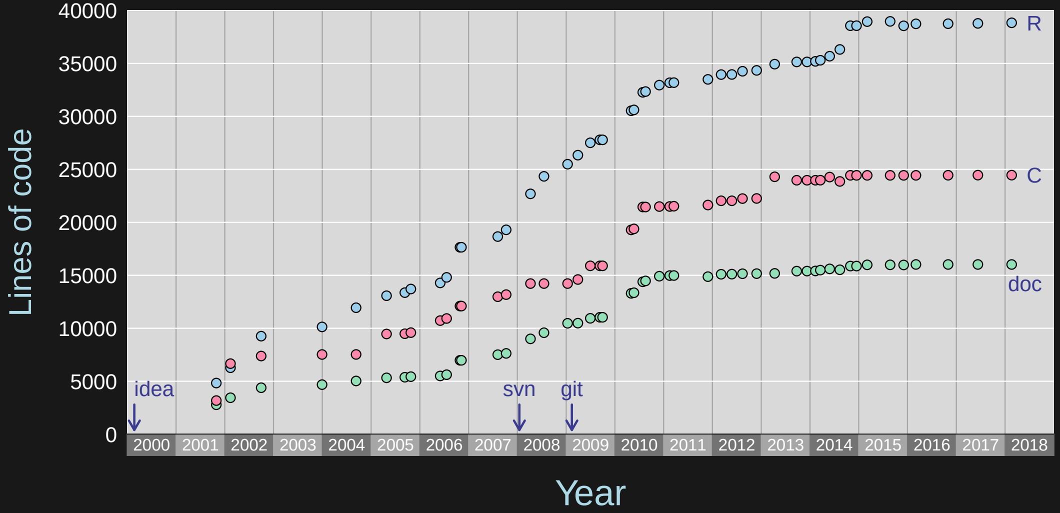
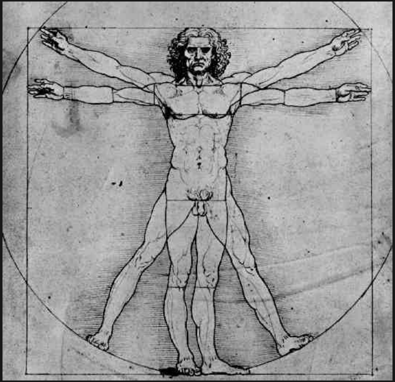
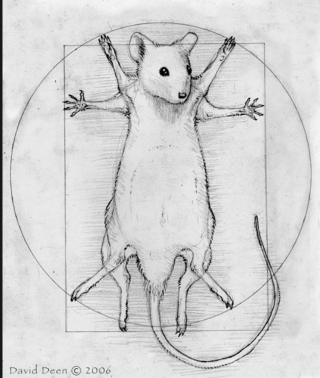
Slides: `bit.ly/rstudio2019`

19 years of R/qtl

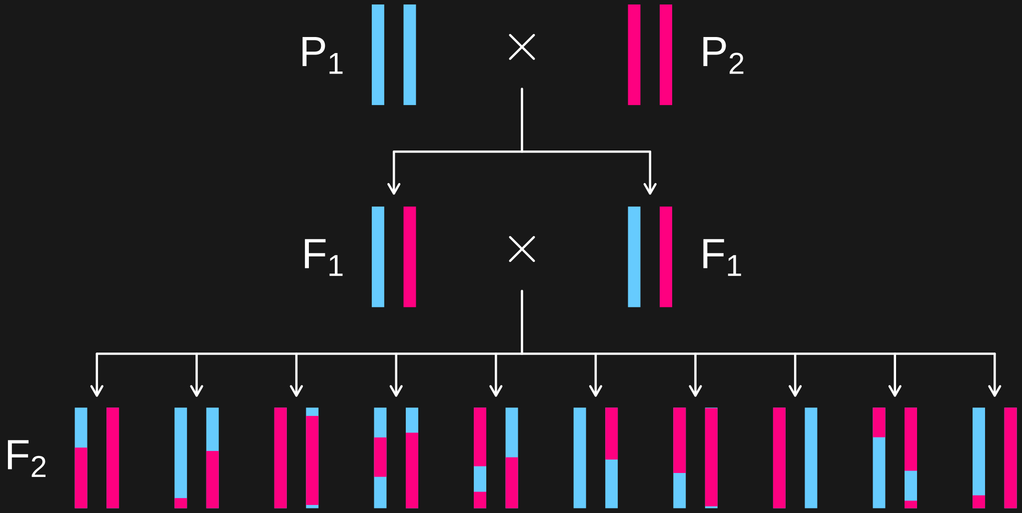




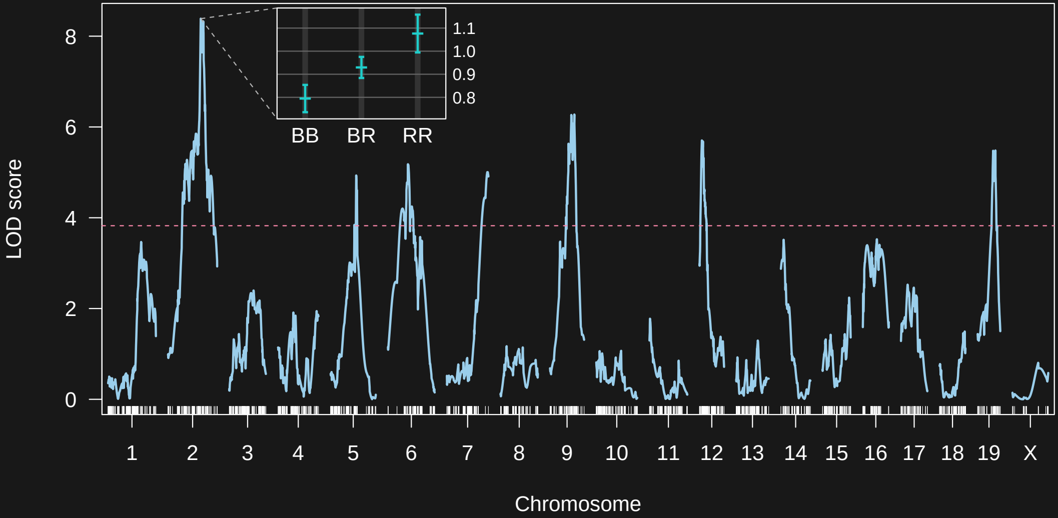


daviddeen.com

Intercross



QTL mapping



LOD score
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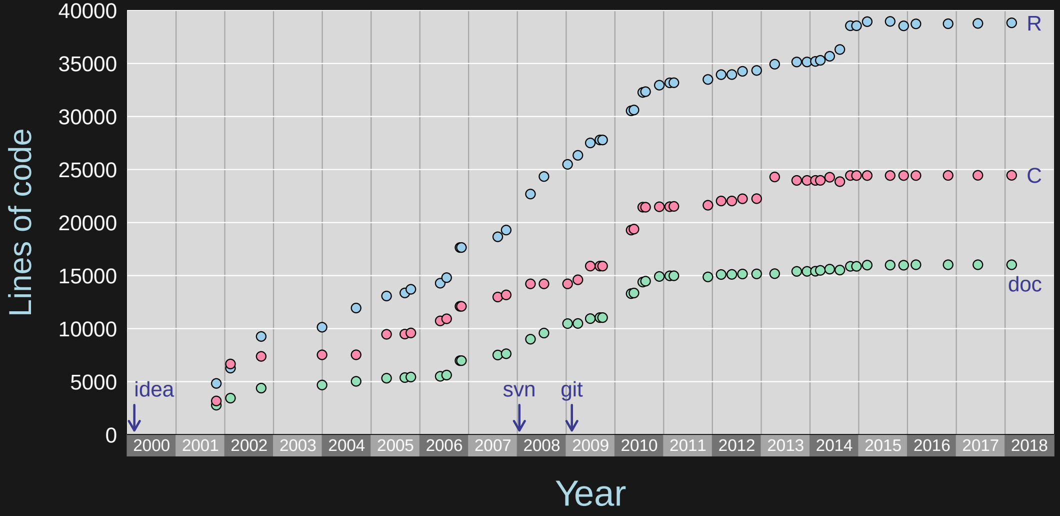
X
Chromosome

19 years of R/qtl



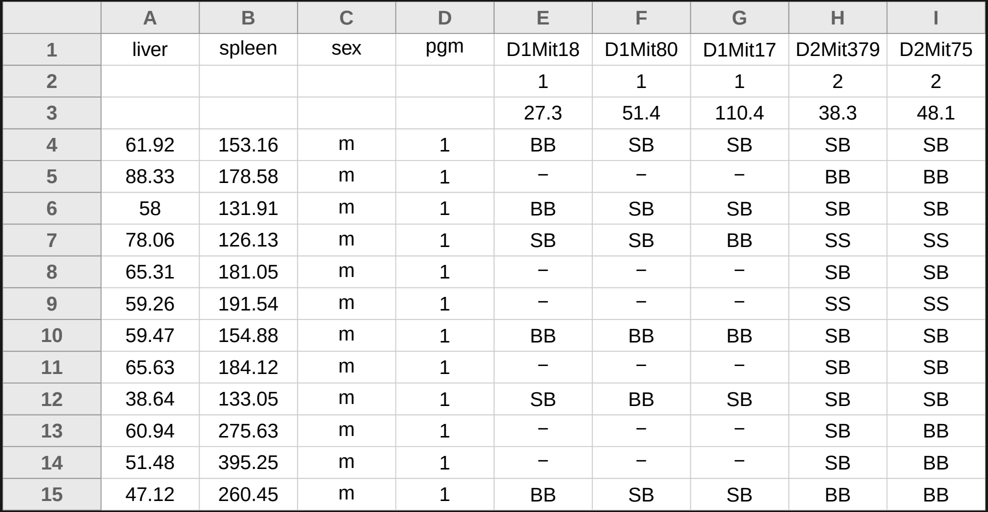
Good things

Good things

- some of the code
- basics of the user interface
- diagnostics and data visualization
- quite comprehensive
- quite flexible

Bad things

Input file



	A	B	C	D	E	F	G	H	I
1	liver	spleen	sex	pgm	D1Mit18	D1Mit80	D1Mit17	D2Mit379	D2Mit75
2					1	1	1	2	2
3					27.3	51.4	110.4	38.3	48.1
4	61.92	153.16	m	1	BB	SB	SB	SB	SB
5	88.33	178.58	m	1	–	–	–	BB	BB
6	58	131.91	m	1	BB	SB	SB	SB	SB
7	78.06	126.13	m	1	SB	SB	BB	SS	SS
8	65.31	181.05	m	1	–	–	–	SB	SB
9	59.26	191.54	m	1	–	–	–	SS	SS
10	59.47	154.88	m	1	BB	BB	BB	SB	SB
11	65.63	184.12	m	1	–	–	–	SB	SB
12	38.64	133.05	m	1	SB	BB	SB	SB	SB
13	60.94	275.63	m	1	–	–	–	SB	BB
14	51.48	395.25	m	1	–	–	–	SB	BB
15	47.12	260.45	m	1	BB	SB	SB	BB	BB

Stupidest code ever

```r
n <- ncol(data)
temp <- rep(FALSE,n)
for(i in 1:n) {
  temp[i] <- all(data[2,1:i]=="")
  if(!temp[i]) break
}
if(!any(temp)) stop("...")
n.phe <- max((1:n)[temp])
```

kbroman.org/blog/2011/08/17/the-stupidest-r-code-ever

Open source means
everyone can see my stupid mistakes

Open source means
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Version control means
everyone can see every stupid mistake I’ve ever made

More typically bad code

The `scantwo()` function is 1446 lines long.

The related C code is 20% of the C code in R/qtl.

Baroque data structures

```
attr(mycross$geno[["X"]]$probs, "map")
```

Inconsistencies

```
plotPXG(mycross, marker="D5M250")

effectplot(mycross, mname1="D5M250")
```

Useless warning messages

```
X'X is singular.
```

Tests

> I don’t need tests; I have users.
>
> – Me

> If you use software that lacks automated tests,
> you are the tests.
>
> – Jenny Bryan

> It’s not that we don’t test our code,
> it’s that we don’t store our tests
> so they can be re-run automatically.
>
> – Hadley Wickham

How did this happen?

- I didn’t know any better
- Not enough re-writing
- Not enough planning
- Personal weaknesses
- Trade-offs (e.g. between interface and data structures)

Documentation

Tailored tutorials >

User guide >

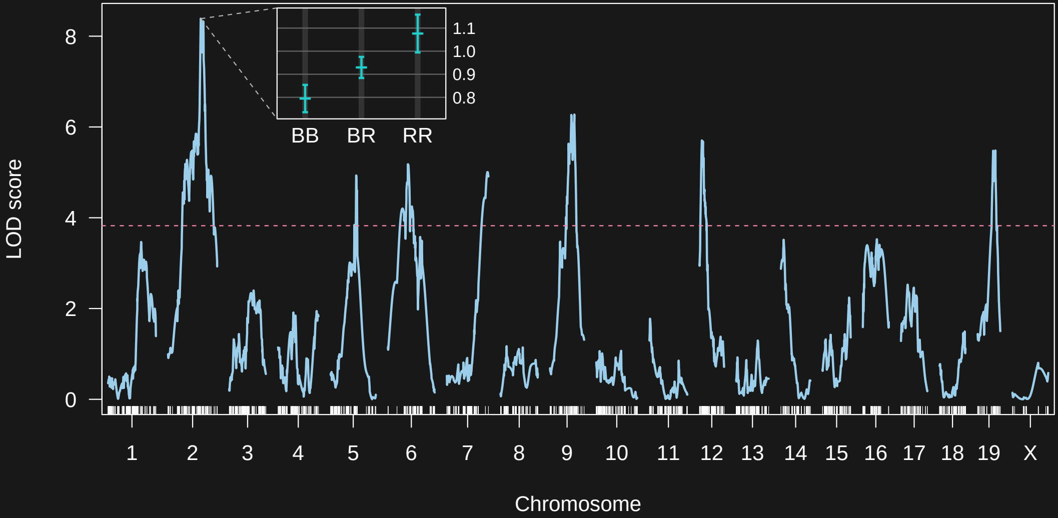
Examples >

Formal documentation

User support

- No question is too insignificant
- Treat each question like it is the first
- Take a breath before responding
- “Send me your data, and I’ll try to figure out what’s going on.”

QTL mapping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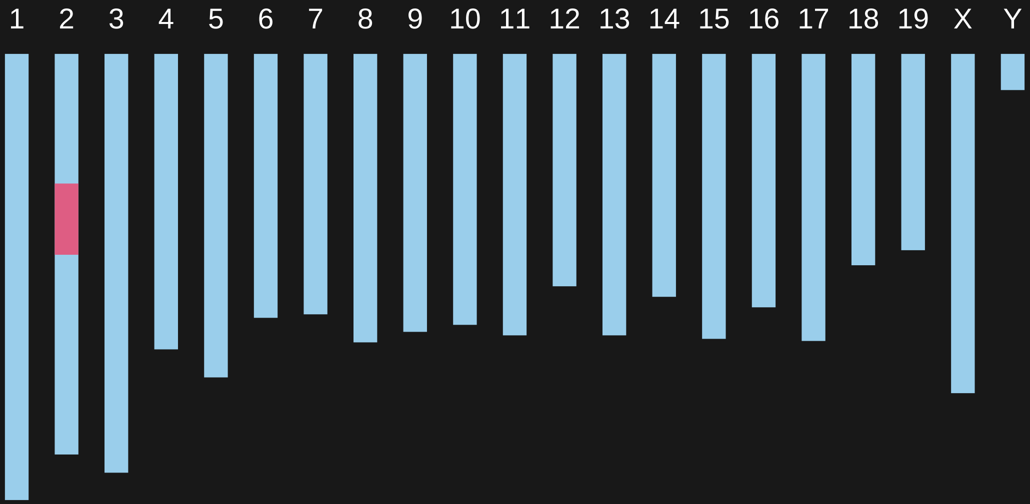
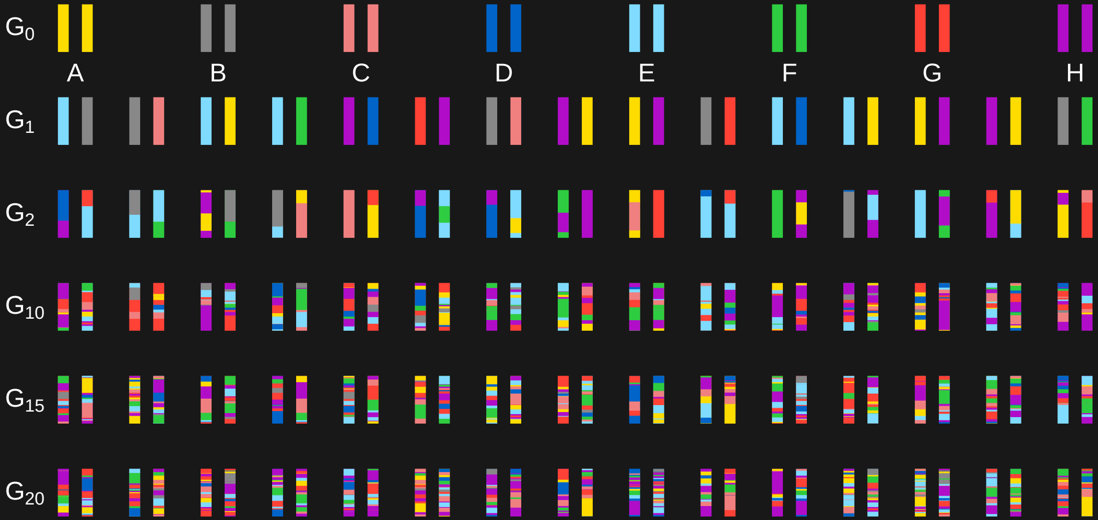
Chromosome

Congenic line



Advanced intercross lines

Heterogeneous stock



Genome-scale phenotypes

Alan Attie

ropenscilabs.github.io/miner_book

R/qtl2

- High-density genotypes
- High-dimensional phenotypes
- Multi-parent populations
- Linear mixed models

`kbroman.org/qtl2`

R/qtl2: Let’s not make the same mistakes

- C++ and Rcpp
- Roxygen2 for documentation
- Unit tests with testthat
- A single “switch” for cross type

R/qtl2: Let’s not make the same mistakes

- C++ and Rcpp
- Roxygen2 for documentation
- Unit tests with testthat
- A single “switch” for cross type
- Yet another data input format
- Flatter data structures, but still complex

Why devote such effort to R/qtl?

- For my own research
- So that others will use my methods ideas
- Has led to numerous collaborations
- I like to be useful

Acknowledgments

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Rohan Shah
Laura Shannon
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Aaron Wolen

NIH/NIGMS

R/qtl users

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